RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/594,908
Source: IFW P
Date Processed by STIC: 10/12/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 10/12/2006
PATENT APPLICATION: **US/10/594,908** TIME: 14:03:47

Input Set : **E:\SEQLIST 11774-006 (as filed).TXT**
Output Set: **N:\CRF4\10122006\J594908.raw**

4 <110> APPLICANT: Wang, Xiangbin
5 Huang, Hualiang
6 Zhao, Baofeng
7 Zhao, Qi
8 Piao, Jinhua
9 Lin, Qing
11 <120> TITLE OF INVENTION: A GENETIC ENGINEERING RECOMBINANT ANTI-CEA, ANTI-CD3
12 AND ANTI-CD28 SINGLE-CHAIN TRI-SPECIFIC ANTIBODY
14 <130> FILE REFERENCE: 11774-006-999 (I040179)
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/594,908
C--> 16 <141> CURRENT FILING DATE: 2006-09-29
16 <150> PRIOR APPLICATION NUMBER: PCT/CN2005/000408
17 <151> PRIOR FILING DATE: 2005-03-29
19 <150> PRIOR APPLICATION NUMBER: CN 200410032158.3
20 <151> PRIOR FILING DATE: 2004-04-01
22 <160> NUMBER OF SEQ ID NOS: 58
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 251
28 <212> TYPE: PRT
29 <213> ORGANISM: Murine
31 <220> FEATURE:
32 <223> OTHER INFORMATION: murine anti-CEA single chain fragment of variable region
33 contained in CEA-scTsAb
35 <400> SEQUENCE: 1

```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
 1               5                  10                  15
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Asp Tyr
            20                  25                  30
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
        35                  40                  45
Gly Glu Ile Leu Pro Gly Ser Gly Arg Thr Asp Tyr Asn Glu Arg Phe
    50                  55                  60
Lys Gly Lys Ala Thr Phe Thr Gly Asp Val Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80
Met Lys Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95
Ala Thr Gly Thr Thr Pro Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110
Thr Val Ser Ala Thr Ser Thr Pro Ser His Asn Ser His Gln Val Pro
        115                 120                 125
Ser Ala Gly Gly Pro Thr Ala Asn Ser Gly Ser Arg Asp Ile Val Leu
```

53 130 135 140

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```
54 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
55 145                 150                 155                 160
56 Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Tyr Thr Tyr
57                 165                 170                 175
58 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
59             180                 185                 190
60 Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
61         195                 200                 205
62 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
63     210                 215                 220
64 Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp Glu Ile Pro Arg
65 225                 230                 235                 240
66 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
67                 245                 250
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 250
72 <212> TYPE: PRT
73 <213> ORGANISM: Murine
75 <220> FEATURE:
76 <223> OTHER INFORMATION: murine anti-CEA single chain fragment of variable
region
77       contained in CEA-scTsAb
79 <400> SEQUENCE: 2
80 Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
81  1               5                  10                  15
82 Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
83             20                  25                  30
84 Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met
85         35                  40                  45
86 Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe
87     50                  55                  60
88 Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
89 65                  70                  75                  80
90 Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
91                 85                  90                  95
92 Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
93             100                 105                 110
94 Gly Ala Gly Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly
95         115                 120                 125
96 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln
97     130                 135                 140
98 Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
99 145                 150                 155                 160
100 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp
101                 165                 170                 175
102 Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr
103             180                 185                 190
104 Ser Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser
105         195                 200                 205
106 Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile
```

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Input Set : **E:\SEQLIST 11774-006 (as filed).TXT**
Output Set: **N:\CRF4\10122006\J594908.raw**

```
107     210                 215                 220
108 Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala
109 225                 230                 235                 240
110 Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala
111                 245                 250
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 2103
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: CEA-scTsAb sequence
122 <400> SEQUENCE: 3
123 atgggtctcg agcaggtgca gctgcagcag agcggtgcgg aactgatgaa accgggcgcg 60
124 agcgtgaaaa tcagctgcaa agcgaccggc tataccttca gcgattattg gatcgaatgg 120
125 gtgaaacagc gtccgggtca cggcctggaa tggatcggtg aaatcctgcc gggcagcggc 180
126 cgtaccgact acaacgaacg tttcaaaggc aaagcgacct tcaccggcga cgtttctagc 240
127 aacaccgcgt atatgaaact gtctagcctg accagcgaag atagcgcggt gtattactgc 300
128 gcgaccggca ccaccccgtt cggttactgg ggtcagggca ccctggttac cgtttccgcg 360
129 actagtaccc cgagccataa cagccatcag gtgccgagcg cgggcggccc gaccgcgaac 420
130 agcggctcta gagacatcgt gctgacccag agcccggcga gcctggcggt gtctctgggt 480
131 cagcgtgcga ccatctcctg ccgtgcttcc cagtccgttt ccacctcctc ctacacctac 540
132 atgcactggt atcagcagaa accgggtcag ccgccgaaac tgctgatcaa atatgcgagc 600
133 aacctggaat ctggtgtgcc ggcgcgtttc agcggttctg gcagcggcac cgacttcacc 660
134 ctgaacatcc acccggtgga agaagaagat accgcgtatt actattgcca gcactcttgg 720
135 gaaatcccgc gtaccttcgg tggcggcacc aaactggaaa tcaaagaatt caacagcacg 780
136 taccgggttg taagcgtcct caccgtactg caccaggact ggctgaatgg caaggaatac 840
137 aaatgcaaga gtactgaggt gaagctggtg gagtctggac ctgagctggt gaagcctgga 900
138 gcttcaatga agatatcctg caaggcttct ggttactcat tcactggcta caccatgaac 960
139 tgggtgaagc agagtcatgg aaagaacctt gagtggatgg gacttattaa tccttacaaa 1020
140 ggtgttagta cctacaacca gaagttcaag gacaaggcca cattaactgt agacaagtca 1080
141 tccagcacag cctacatgga actcctcagt ctgacatctg aggactctgc agtctattac 1140
142 tgtgcaagat cggggtacta cggtgatagt gactggtact tcgatgtctg gggcgcagga 1200
143 acctcagtca ctgtctcctc aactagtggt ggtggtggtt ctggtggtgg tggttctggt 1260
144 ggtggtggtt cttctagaga catccagatg acccagacca catcctccct gtctgcctct 1320
145 ctgggagaca gagtcaccat cagttgcagg gcaagtcagg acattagaaa ttatttaaac 1380
146 tggtatcaac agaaaccaga tggaactgtt aaactcctga tctactacac atcaagatta 1440
147 cactcaggag tcccatcaaa gttcagtggc agtgggtctg gaacagatta ttctctcacc 1500
148 attagcaacc tggagcaaga ggatattgcc acttactttt gccaacaggg taatacgctt 1560
149 ccgtggacgt tcgctggagg caccaaactg gaactgaagc gcgctgtcga cttccagaat 1620
150 gcgctgctgg ttcgttacac caagaaagta ccccaagtgt caactccaac tcctgtagag 1680
151 gtctcacata tgcaggtaca gctacaggaa tctggtccgg gtctggtaaa accgtctcag 1740
152 accctgtctc tgacctgtac cgtatctggt ttctctctgt ctgactatgg tgttcattgg 1800
153 gtacgtcagc cgccaggtaa aggtctggaa tgtctgggtg taatatgggg tggaggcacg 1860
154 aattataatt cggctctcat gtccagacgt gtaacctctt ccgacgatac ctctaaaaat 1920
155 cagttctctc tgaaactgtc ttccgtagac accgctgtat actattgtgc tcgttcctat 1980
156 tactattcta tggactactg gggtcagggc accctggtaa ccgtatcttc cggtaccgaa 2040
157 caaaaactca tctcagaaga ggatctgaat ggggccgcac atcatcatca ccatcacgag 2100
158 caa                                                              2103
160 <210> SEQ ID NO: 4
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RAW SEQUENCE LISTING DATE: 10/12/2006
PATENT APPLICATION: **US/10/594,908** TIME: 14:03:47

Input Set : **E:\SEQLIST 11774-006 (as filed).TXT**
Output Set: **N:\CRF4\10122006\J594908.raw**

<211> LENGTH: 701
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: CEA-scTsAb sequence
<400> SEQUENCE: 4

```
Met Gly Leu Glu Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met
 1               5                  10                  15
Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr
            20                  25                  30
Phe Ser Asp Tyr Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly
        35                  40                  45
Leu Glu Trp Ile Gly Glu Ile Leu Pro Gly Ser Gly Arg Thr Asp Tyr
    50                  55                  60
Asn Glu Arg Phe Lys Gly Lys Ala Thr Phe Thr Gly Asp Val Ser Ser
65                  70                  75                  80
Asn Thr Ala Tyr Met Lys Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
                85                  90                  95
Val Tyr Tyr Cys Ala Thr Gly Thr Thr Pro Phe Gly Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ala Thr Ser Thr Pro Ser His Asn Ser
        115                 120                 125
His Gln Val Pro Ser Ala Gly Gly Pro Thr Ala Asn Ser Gly Ser Arg
    130                 135                 140
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
145                 150                 155                 160
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
                165                 170                 175
Ser Tyr Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
            180                 185                 190
Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
        195                 200                 205
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
    210                 215                 220
Pro Val Glu Glu Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp
225                 230                 235                 240
Glu Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu
                245                 250                 255
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            260                 265                 270
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Ser Thr Glu Val Lys
        275                 280                 285
Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys
    290                 295                 300
Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
305                 310                 315                 320
Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile
                325                 330                 335
Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys
```

```
212                 340                 345                 350
213 Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu
214         355                 360                 365
215 Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser
216     370                 375                 380
217 Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly
218 385                 390                 395                 400
219 Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly Ser Gly Gly
220                 405                 410                 415
221 Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln Met Thr Gln
222                 420                 425                 430
223 Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser
224         435                 440                 445
225 Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln
226     450                 455                 460
227 Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu
228 465                 470                 475                 480
229 His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp
230                 485                 490                 495
231 Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr
232                 500                 505                 510
233 Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr
234         515                 520                 525
235 Lys Leu Glu Leu Lys Arg Ala Val Asp Phe Gln Asn Ala Leu Leu Val
236     530                 535                 540
237 Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Pro Val Glu
238 545                 550                 555                 560
239 Val Ser His Met Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
240                 565                 570                 575
241 Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser
242                 580                 585                 590
243 Leu Ser Asp Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly
244         595                 600                 605
245 Leu Glu Cys Leu Gly Val Ile Trp Gly Gly Gly Thr Asn Tyr Asn Ser
246     610                 615                 620
247 Ala Leu Met Ser Arg Arg Val Thr Ser Ser Asp Asp Thr Ser Lys Asn
248 625                 630                 635                 640
249 Gln Phe Ser Leu Lys Leu Ser Ser Val Asp Thr Ala Val Tyr Tyr Cys
250                 645                 650                 655
251 Ala Arg Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Leu
252             660                 665                 670
253 Val Thr Val Ser Ser Gly Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp
254         675                 680                 685
255 Leu Asn Gly Ala Ala His His His His His His Glu Gln
256     690                 695                 700
259 <210> SEQ ID NO: 5
260 <211> LENGTH: 18
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
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VERIFICATION SUMMARY DATE: 10/12/2006
PATENT APPLICATION: **US/10/594,908** TIME: 14:03:49

Input Set : **E:\SEQLIST 11774-006 (as filed).TXT**
Output Set: **N:\CRF4\10122006\J594908.raw**

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date